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7148.003 Sequence Listing.ST25
SEQUENCE LISTING

<110> Cummings, Richard D.
Ju, Tongzhong

<120> CORE1 BETA-3 GALACTOSYLTRANSFERASE SPECIFIC MOLECULAR
CHAPARONES, NUCLEIC ACIDS, AND METHODS OF USE THEREOF

<130> 7148.003

<150> 60/411,310

<151> 2002-09-13

<160> 16

<170> PatentIn version 3.1

<210> 1

<211> 318

<212> PRT

<213> Homo sapiens

<400> 1

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1 5 10 15

Ile Phe Cys Ala Leu Ile Thr Met Leu Gly His Ile Arg Ile Gly His
20 25 30

Gly Asn Arg Met His His His Glu His His His Leu Gln Ala Pro Asn
35 40 45

Lys Glu Asp Ile Leu Lys Ile Ser Glu Asp Glu Arg Met Glu Leu Ser
50 55 60

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Lys Ser Phe Arg Val Tyr Cys Ile Ile Leu Val Lys Pro Lys Asp Val
65 70 75 80

Ser Leu Trp Ala Ala Val Lys Glu Thr Trp Thr Lys His Cys Asp Lys
85 90 95

Ala Glu Phe Phe Ser Ser Glu Asn Val Lys Val Phe Glu Ser Ile Asn
100 105 110

Met Asp Thr Asn Asp Met Trp Leu Met Met Arg Lys Ala Tyr Lys Tyr
115 120 125

Ala Phe Asp Lys Tyr Arg Asp Gln Tyr Asn Trp Phe Phe Leu Ala Arg
130 135 140

Pro Thr Thr Phe Ala Ile Ile Glu Asn Leu Lys Tyr Phe Leu Leu Lys
145 150 155 160

Lys Asp Pro Ser Gln Pro Phe Tyr Leu Gly His Thr Ile Lys Ser Gly
165 170 175

Asp Leu Glu Tyr Val Gly Met Glu Gly Gly Ile Val Leu Ser Val Glu
180 185 190

Ser Met Lys Arg Leu Asn Ser Leu Leu Asn Ile Pro Glu Lys Cys Pro
195 200 205

Glu Gln Gly Gly Met Ile Trp Lys Ile Ser Glu Asp Lys Gln Leu Ala
210 215 220

Val Cys Leu Lys Tyr Ala Gly Val Phe Ala Glu Asn Ala Glu Asp Ala
225 230 235 240

Asp Gly Lys Asp Val Phe Asn Thr Lys Ser Val Gly Leu Ser Ile Lys
245 250 255

Glu Ala Met Thr Tyr His Pro Asn Gln Val Val Glu Gly Cys Cys Ser
260 265 270

Asp Met Ala Val Thr Phe Asn Gly Leu Thr Pro Asn Gln Met His Val
275 280 285

Met Met Tyr Gly Val Tyr Arg Leu Arg Ala Phe Gly His Ile Phe Asn

290

295

300

Asp Ala Leu Val Phe Leu Pro Pro Asn Gly Ser Asp Asn Asp
 305 310 315

<210> 2

<211> 957

<212> DNA

<213> Homo sapiens

<400> 2

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catcatcacc tacaagctcc taacaaagaa gatatcttga aaatttcaga ggatgagcgc      180
atggagctca gtaagagctt tcgagtatac tgtattatcc ttgtaaaacc caaagatgtg      240
agtctttggg ctgcagtaaa ggagacttgg accaaacact gtgacaaagc agagttcttc      300
agttctgaaa atgttaaagt gtttgagtca attaatatgg acacaaatga catgtgggta      360
atgatgagaa aagcttacia atacgccttt gataagtata gagaccaata caactgggtc      420
ttccttgcac gcccactac gtttgctatc attgaaaacc taaagtatct tttgttaaaa      480
aaggatccat cacagccttt ctatctaggc cacactataa aatctggaga ccttgaatat      540
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ctcaatatcc cagaaaagtg tcctgaacag ggagggatga tttggaagat atctgaagat      660
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gatggaaaag atgtatttaa taccaaactc gttgggcttt ctattaaaga ggcaatgact      780
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ctgactccaa atcagatgca tgtgatgatg tatgggggat accgccttag ggcatttggg      900
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<210> 3

<211> 316

<212> PRT

<213> Mus musculus

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<400> 3

Met Leu Ser Glu Ser Ser Ser Phe Leu Lys Gly Val Met Leu Gly Ser
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Ile Phe Cys Ala Leu Ile Thr Met Leu Gly His Ile Arg Ile Gly Asn
 20 25 30

Arg Met His His His Glu His His His Leu Gln Ala Pro Asn Lys Asp
 35 40 45

Asp Ile Ser Lys Ile Ser Glu Ala Glu Arg Met Glu Leu Ser Lys Ser
 50 55 60

Phe Arg Val Tyr Cys Ile Val Leu Val Lys Pro Lys Asp Val Ser Leu
 65 70 75 80

Trp Ala Ala Val Lys Glu Thr Trp Thr Lys His Cys Asp Lys Ala Glu
 85 90 95

Phe Phe Ser Ser Glu Asn Val Lys Val Phe Glu Ser Ile Asn Met Asp
 100 105 110

Thr Asn Asp Met Trp Leu Met Met Arg Lys Ala Tyr Lys Tyr Ala Tyr
 115 120 125

Asp Gln Tyr Arg Asp Gln Tyr Asn Trp Phe Phe Leu Ala Arg Pro Thr
 130 135 140

Thr Phe Ala Val Ile Glu Asn Leu Lys Tyr Phe Leu Leu Lys Lys Asp
 145 150 155 160

Gln Ser Gln Pro Phe Tyr Leu Gly His Thr Val Lys Ser Gly Asp Leu
 165 170 175

Glu Tyr Val Ser Val Asp Gly Gly Ile Val Leu Ser Ile Glu Ser Met
 180 185 190

Lys Arg Leu Asn Ser Leu Leu Ser Val Pro Glu Lys Cys Pro Glu Gln
 195 200 205

Gly Gly Met Ile Trp Lys Ile Ser Glu Asp Lys Gln Leu Ala Val Cys
 210 215 220

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Leu Lys Tyr Ala Gly Val Phe Ala Glu Asn Ala Glu Asp Ala Asp Gly
225 230 235 240

Lys Asp Val Phe Asn Thr Lys Ser Val Gly Leu Phe Ile Lys Glu Ala
245 250 255

Met Thr Asn Gln Pro Asn Gln Val Val Glu Gly Cys Cys Ser Asp Met
260 265 270

Ala Val Thr Phe Asn Gly Leu Thr Pro Asn Gln Met His Val Met Met
275 280 285

Tyr Gly Val Tyr Arg Leu Arg Ala Phe Gly His Val Phe Asn Asp Ala
290 295 300

Leu Val Phe Leu Pro Pro Asn Gly Ser Glu Asn Asp
305 310 315

<210> 4

<211> 1432

<212> DNA

<213> Mus musculus

<400> 4

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gtgatgcttg gaagcatctt ctgtgccttg atcactatgc taggccacat taggattgga	180
aacagaatgc accaccatga gcatcaccat ctgcaagccc ctaacaaaga cgatatctcg	240
aaaatttcag aggctgaacg catggagctc agtaagagtt tccgggtata ctgtatagtt	300
cttgtaaaac ccaaagatgt gagtctttgg gctgcagtga aggagacttg gaccaaacac	360
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gacacaaatg acatgtgggt gatgatgagg aaagcttaca aatatgctta tgatcaatac	480
agggaccaat acaactgggt cttccttgca cgccccacta ctttcgctgt tattgaaaac	540
ctcaaatatt ttttgtaaa aaaggatcaa tccaacctt tctatctcgg acacactgta	600
aaatctggag accttgaata tgtgagtgtg gatggaggaa ttgtcttaag catagaatca	660
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ttcattaaag aggcaatgac taaccaacca aaccaggtag tagaaggctg ttgctctgat    900
atggctgtta ctttcaatgg actgactcct aatcagatgc acgtgatgat gtatggggtg    960
taccggctta gggcatttgg acatgttttc aatgatgcat tggttttcctt acctccaaat   1020
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gtatcatttt taattgatga cagatctaac atagtaatat gattcttttt cttatctttt   1140
accattgaa gtctgcttgt acaatgtcaa atggaatgct gtttttcctt tatatcattc   1200
ctgagaaatt aaaatgtatt aaaaataaat gttttaaaaa tagcaatttt tcaaacacat   1260
atttataagt atatttatgt gataaagact aaattataga cattgtaatc tgtggtgtat   1320
ctttgcttat tggttttaaa cttatgtatc attttagctt tgtaatatat gtaaagaga   1380
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<210> 5

<211> 313

<212> PRT

<213> Brachydanio rerio

<400> 5

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Ile Phe Cys Leu Ile Met Ser Phe Phe Glu Thr Phe Asn Pro Gly Thr
20          25          30

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His Ser Glu Gly His Asn His Leu His His His Leu Lys Pro Val Ser
35          40          45

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Lys Asp Glu Leu Gln Lys Leu Ser Glu Ser Gln Met Ser Glu Phe Ala
50          55          60

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Met Gln Val Arg Val Tyr Cys Leu Ile Met Val Thr Pro Lys Leu Leu
65          70          75          80

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Val His Trp Ala Thr Ala Asn Asp Thr Trp Ser Lys His Cys Asp Lys

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Ser Val Phe Tyr Thr Ser Glu Ala Ser Lys Ala Leu Asp Ala Val Asp
100 105 110

Leu Gln Glu Gln Asp Glu Trp Thr Arg Leu Arg Lys Ala Ile Gln His
115 120 125

Ala Tyr Glu Asn Ala Gly Asp Leu His Trp Phe Phe Ile Ala Arg Pro
130 135 140

Thr Thr Phe Ala Ile Ile Glu Asn Leu Lys Tyr Leu Val Leu Asp Lys
145 150 155 160

Asp Pro Ser Gln Pro Phe Tyr Ile Gly His Thr Glu Lys Ser Gly Glu
165 170 175

Leu Asp Tyr Val Glu Tyr Asp Ser Gly Ile Val Leu Ser Tyr Glu Ala
180 185 190

Met Arg Arg Leu Met Glu Val Phe Lys Asp Glu Asp Lys Cys Pro Glu
195 200 205

Arg Gly Arg Ala Leu Trp Lys Met Ser Glu Glu Lys Gln Leu Ala Thr
210 215 220

Cys Leu Lys Tyr Ser Gly Val Phe Ala Glu Asn Gly Glu Asp Ala Gln
225 230 235 240

Gly Lys Gly Leu Phe Asn Lys Lys Ser Val Ser Ser Leu Ile Ser Asp
245 250 255

Ser Ile Ser Gln Asn Pro Gly Asp Val Val Glu Ala Cys Cys Ser Asp
260 265 270

Met Ala Ile Thr Phe Ala Gly Met Ser Pro Ser Gln Ile Gln Val Leu
275 280 285

Met Tyr Gly Val Tyr Arg Leu Arg Pro Tyr Gly His Asp Phe His Asp
290 295 300

Ser Leu Thr Phe Leu Pro Pro Arg Leu
305 310

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<210> 6

<211> 1223

<212> DNA

<213> Brachydanio rerio

<400> 6

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gtcagcaaag atgagctaca gaagttatcc gagtctcaga tgtctgagtt cgctatgcag	240
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aacgacacct ggagcaaaca ctgcgacaaa tctgtgtttt acacctctga ggcgctctaaa	360
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tacattggcc acacggaaaa gtctggagag ctggattatg tggagtacga cagtgggatt	600
gtgttgagtt atgaagcgat gaggaggctg atggagggtg ttaaagatga agataaatgt	660
ccagagcgag gacgagctct atggaagatg tctgaagaaa agcaactggc cacttgtctg	720
aagtacagcg gagtgtttgc tgaaaacgga gaggacgccc aaggcaaagg gctttttaac	780
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<210> 7

<211> 316

<212> PRT

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<213> Rattus norvegicus

<400> 7

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Arg	Met	His	His	His	Glu	His	His	His	Leu	Gln	Ala	Pro	Asn	Lys	Asp	35	40	45	
Asp	Ile	Leu	Lys	Ile	Ser	Glu	Thr	Glu	Arg	Met	Glu	Leu	Ser	Lys	Ser	50	55	60	
Phe	Gln	Val	Tyr	Cys	Ile	Val	Leu	Val	Lys	Pro	Lys	Asp	Val	Ser	Leu	65	70	75	80
Trp	Ala	Ala	Val	Lys	Glu	Thr	Trp	Thr	Lys	His	Cys	Asp	Lys	Ala	Glu	85	90	95	
Phe	Phe	Ser	Ser	Glu	Asn	Val	Lys	Val	Phe	Glu	Ser	Ile	Asn	Met	Asp	100	105	110	
Thr	Asn	Asp	Met	Trp	Leu	Met	Met	Arg	Lys	Ala	Tyr	Lys	Tyr	Ala	Tyr	115	120	125	
Asp	Lys	Tyr	Lys	Asp	Gln	Tyr	Asn	Trp	Phe	Phe	Leu	Ala	Arg	Pro	Thr	130	135	140	
Thr	Phe	Ala	Val	Ile	Glu	Asn	Leu	Lys	Tyr	Phe	Leu	Leu	Arg	Lys	Asp	145	150	155	160
Pro	Ser	Gln	Pro	Phe	Tyr	Leu	Gly	His	Thr	Val	Lys	Ser	Gly	Asp	Leu	165	170	175	
Glu	Tyr	Val	Ser	Val	Asp	Gly	Gly	Ile	Val	Leu	Ser	Ile	Glu	Ser	Met	180	185	190	
Lys	Arg	Leu	Asn	Gly	Leu	Leu	Ser	Val	Pro	Glu	Lys	Cys	Pro	Glu	Gln	195	200	205	

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Gly Gly Met Ile Trp Lys Ile Ser Glu Asp Lys Gln Leu Ala Val Cys
210 215 220

Leu Lys Tyr Ala Gly Val Phe Ala Glu Asn Ala Glu Asp Ala Asp Gly
225 230 235 240

Lys Asp Val Phe Asn Thr Lys Ser Val Gly Leu Phe Ile Lys Glu Ala
245 250 255

Met Thr Asn Gln Pro Asn Gln Val Val Glu Gly Cys Cys Ser Asp Met
260 265 270

Ala Val Thr Phe Asn Gly Leu Thr Pro Asn Gln Met His Val Met Met
275 280 285

Tyr Gly Val Tyr Arg Leu Arg Ala Phe Gly His Val Phe Asn Asp Ala
290 295 300

Leu Val Phe Leu Pro Pro Asn Gly Ser Glu Asn Asp
305 310 315

<210> 8

<211> 1283

<212> DNA

<213> Rattus norvegicus

<400> 8

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gagtcaatta atatggacac aaatgatatg tggttgatga tgaggaaagc ttacaaatat	300
gcttatgata aatacaagga ccaatacaac tggttcttcc ttgcacgccc cactactttc	360
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gaacaaggag gaatgatttg gaagatatct gaagataagc agctagcagt ctgcctgaaa	600

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TTTTtcttat ctggTtacac tggTataatc acacattgaa gtctactTgt acattgtcaa	1020
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TTTtaagaat aacaattTTTt caaatacata tttataaata ctatatttat gtgataaaga	1140
ctaaattata gacattaaaa tctgtggTgt atctttgctt attggTTTta tacctgtgta	1200
ttggggTtg ggatttagct cagtggtaga gtgcttgctt agcaagcgca aggcctggg	1260
TTTggtcctt acctccgagg gaa	1283

<210> 9

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Completely synthesized.

<400> 9

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<210> 10

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Completely synthesized.

<400> 10

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<210> 11

<211> 22

<212> DNA

<213> Artificial sequence

<220>

<223> Completely synthesized.

<400> 11

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<210> 12

<211> 69

<212> DNA

<213> Artificial sequence

<220>

<223> Completely synthesized.

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tcacttttg

69

<210> 13

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> Completely synthesized.

<400> 13

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5

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<210> 14

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<223> Completely synthesized.

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<210> 15

<211> 18

<212> PRT

<213> Artificial sequence

<220>

<223> Completely synthesized.

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Met Leu Ser Glu Ser Ser Ser Phe Leu Lys Gly Val Met Leu Gly Ser
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Ile Phe

<210> 16

<211> 7

<212> PRT

<213> Artificial sequence

<220>

<223> Completely synthesized.

<400> 16

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